

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2002, 17:40:15 ; Search time 63.43 Seconds

(without alignments)
575.468 Million cell updates/sec

Title: US-09-502-984B-6

Perfect score: 1098

Sequence: 1 KFESKALLAARGPPELLCF.....AEPFGGFWMSMSEPVSLTT 211

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_trembl_19.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mhc.*
9: sp_organelle.*
10: sp_phage.*
11: sp_plant.*
12: sp_rodent.*
13: sp_virus.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	903.5	82.3	509	Q9MYZ9	Q9MYZ9 sus scrofa
2	877.5	79.9	316	11 Q35545	Q35545 rattus norv
3	782	71.2	229	6 Q27950	Q27950 bos indicus
4	778	70.9	6	Q28206	Q28206 bos taurus
5	719.5	65.5	387	6 Q95N13	Q95N13 ovis aries
6	719.5	65.5	418	6 Q95N14	Q95N14 ovis aries
7	152	13.8	566	11 Q925F5	Q925F5 mus musculu
8	122.5	11.2	422	4 Q75462	Q75462 homo sapien
9	121.5	11.1	422	4 Q90H5	Q90H5 homo sapien
10	119.5	10.9	296	6 Q18880	Q18880 mus musculu
11	118	10.7	6	Q9JMS8	Q9JMS8 bos taurus
12	112.5	10.2	581	6 Q46561	Q46561 ovis aries
13	112.5	10.2	634	6 Q46600	Q46600 bos taurus
14	111.5	10.2	626	13 Q90WC7	Q90WC7 cynops pyrr
15	111	10.1	521	4 Q96TF0	Q96TF0 homo sapien
16	105.5	9.6	638	6 Q95JF2	Q95JF2 alluropoda

17	104.5	9.5	608	6 Q9NOY7	Q9NOY7 monodelphis
18	102.5	9.3	628	11 Q9JKT1	Q9JKT1 cavia porce
19	102.5	9.3	628	11 Q9JKT1	Q9JKT1 cavia porce
20	102.5	9.3	628	11 Q9JKT1	Q9JKT1 cavia porce
21	101.5	9.2	848	6 Q9M2S2	Q9M2S2 sus scrofa
22	99.5	9.1	1165	6 Q02671	Q02671 sus scrofa
23	99	9.0	622	6 Q9NOJ7	Q9NOJ7 callithrix
24	99	9.0	894	6 Q9MYL1	Q9MYL1 macaca mula
25	99	9.0	925	6 Q9MYK9	Q9MYK9 macaca mula
26	99	9.0	1163	6 Q9MYL2	Q9MYL2 macaca mula
27	99	9.0	1194	6 Q9MYL0	Q9MYL0 macaca mula
28	98	8.9	538	4 Q9HBE5	Q9HBE5 homo sapien
29	98	8.9	538	4 Q9HB91	Q9HB91 homo sapien
30	96.5	8.8	390	4 Q9UEH7	Q9UEH7 homo sapien
31	96.5	8.8	638	6 Q9YU69	Q9YU69 canis famill
32	96.5	8.8	1093	11 Q70535	Q70535 rattus norv
33	96	8.7	896	4 Q92919	Q92919 homo sapien
34	96	8.7	896	4 Q13594	Q13594 homo sapien
35	96	8.7	906	4 Q13593	Q13593 homo sapien
36	96	8.7	958	4 Q92920	Q92920 homo sapien
37	96	8.7	958	4 Q13592	Q13592 homo sapien
38	96	8.7	1165	4 Q92921	Q92921 homo sapien
39	95.5	8.7	611	13 Q9PTR9	Q9PTR9 xenopus lae
40	95.5	8.7	636	13 Q90216	Q90216 parailichthy
41	94.5	8.6	615	13 Q9DE35	Q9DE35 pelodiscus
42	94.5	8.6	632	6 Q95ML5	Q95ML5 salmirl hol
43	93	8.5	227	6 Q9GLW3	Q9GLW3 ursus marit
44	91	8.3	608	11 Q99JZ1	Q99JZ1 mus musculu
45	90	8.2	229	4 Q14213	Q14213 homo sapien

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	509 AA.
Q9MYZ9	Q9MYZ9			
AC	Q9MYZ9:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	ERYTHROPOIETIN RECEPTOR.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RA	Pearson P.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G.,			
RA	Christenson R.K., Vallet J.L.,			
RT	"Porcine Erythropoietin Receptor: Molecular Cloning and Expression in			
RT	Embryonic and Fetal Liver."			
RL	Domest. Anim. Endocrinol. 0:0-0(2000).			
DR	EMBL: AF274305; AAF77065.1; -			
DR	HSSP: P19235; IEBA.			
DR	InterPro: IPR002986; CRIA.			
DR	InterPro: IPR000572; Euk_oxidored_molyb.			
DR	InterPro: IPR003961; FN_III.			
DR	InterPro: IPR003528; Hematopo_receptor_L_F1.			
DR	Pfam: PF00041; fn3. 1.			
DR	SMART: SM00060; FN3. 1.			
DR	PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.			
DR	PROSITE: PS00559; MOLYBDOPTERIN_EUK; UNKNOWN_1.			
DR	RECEPTOR.			
SQ	SEQUENCE 509 AA; 55183 MW; 35B565D07C6BCD8A CRC64;			

Query Match 82.3%; Score 903.5; DB 6; Length 509;
Best Local Similarity 80.2%; Pred. No. 3.7e-79;
Matches 170; Conservative 18; Mismatches 23; Indels 1; Gaps 1;
QY 1 KFESKALLAARGPPELLCFTEHRLDLVCFPEEASAGVPGNFSFQLDEDPMLICRL 60

```

Db 34 KFEKKAALLAARGPEELCFERLEDVCFWEFAGSAGVGEDYSFSYQLEGEPWKCRL 93
QY 61 HOAPTANGAIRFWCSLTADTSSVPLELRT-AASGAPRHRVHINEVLLDAPGLV 119
Db 94 HOGTANGSVRFWCSLTADTSSVPLELRTVEVSGAPRHRVHINEVLLDAPGLL 153
QY 120 ARLADESGHVIRWLPPEPTMTSHIRELDISANGAGSVORVELLEGRTCVLSNLRG 179
Db 154 ARRAEESGHVLRWLPPEGAPMALLIREVNIITREMAAGVQREIILDGRTCVLSNLRG 213
QY 180 TRITIAVRARMAEPSPFGFWSAMSEPVSLT 211
Db 214 GTRTYFMVRRARMAEPSPFGFWSAMSEPVSLT 245

RESULT 2
ID 035545 PRELIMINARY; PRT; 316 AA.
AC 035545;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE INTRON 5-INSERTED FORM OF ERYTHROPOIETIN RECEPTOR PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98296111; PubMed=9630610;
RA Yamaqi R., Murakami C., Takenoshita M., Tsuyama S., Inui H.,
RA Miyatake K., Nakano Y.;
RT "The intron 5-inserted form of rat erythropoietin receptor is
RT expressed as a membrane-bound form.";
RL Biochim. Biophys. Acta 1403:169-178(1998).
DR EMBL: D83509; BAA22373.1; -.
DR HSSP: P19235; IEBA.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 316 POTENTIAL.
SQ SEQUENCE 316 AA; 34220 MW; 05C44BF8516C180B CRC64;

```

Query Match 79.9%; Score 877.5; DB 11; Length 316;
 Best Local Similarity 78.2%; Pred. No. 6.8e-77;
 Matches 165; Conservative 22; Mismatches 22; Indels 1; Gaps 1;

```

QY 1 KFEKKAALLAARGPEELCFERLEDVCFWEFAGSAGVGEDYSFSYQLEGEPWKCRL 60
Db 34 KFEKKAALLAARGPEELCFERLEDVCFWEFAGSAGVGEDYSFSYQLEGEPWKCRL 92
QY 61 HOAPTANGAIRFWCSLTADTSSVPLELRTAASGAPRHRVHINEVLLDAPGLV 120
Db 94 HOGTANGSVRFWCSLTADTSSVPLELRTVEVSGAPRHRVHINEVLLDAPGLL 152
QY 121 ARLADESGHVIRWLPPEPTMTSHIRELDISANGAGSVORVELLEGRTCVLSNLRG 180
Db 154 ARRAEESGHVLRWLPPEGAPMALLIREVNIITREMAAGVQREIILDGRTCVLSNLRG 212
QY 181 TRITIAVRARMAEPSPFGFWSAMSEPVSLT 211
Db 214 GTRTYFMVRRARMAEPSPFGFWSAMSEPVSLT 243

RESULT 3
QY 027950 PRELIMINARY; PRT; 229 AA.
AC 027950;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RX [1]
RP SEQUENCE FROM N.A.
RA TISSUE=BONE MARROW;
RA Suliman H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61399; AAB03871.1; -.
DR HSSP: P19235; IEBA.

```

```

ID 027950 PRELIMINARY; PRT; 229 AA.
AC 027950;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RX [1]
RP SEQUENCE FROM N.A.
RA TISSUE=BONE MARROW;
RA Suliman H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61399; AAB03870.1; -.
DR HSSP: P19235; IEBA.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 229 229
SQ SEQUENCE 229 AA; 25196 MW; F6E01CAAB07893E8 CRC64;

```

Query Match 71.2%; Score 782; DB 6; Length 229;
 Best Local Similarity 78.5%; Pred. No. 8.1e-68;
 Matches 146; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

```

QY 26 DLVCFEEFASAGVCPNFSFQLEDEPWLKCLHQAPTARGAIRRWCSLPTADTSSV 85
Db 1 DLVCFEWEBAATAGVGPVNSFSYQLEGEPMKPCRLHQAPTARGLVRFWCSLPTADTSSV 60
QY 86 PLELRTAASGAPRHRVHINEVLLDAPGLVARLADESGHVIRWLPPEPTMTSHI 145
Db 61 PLELHTAASGASKRRTIHINEVLLDAPPARLVARRADESGHVLRWLPPEGAPMALLI 120
QY 146 REFELDISANGAGSVORVELLEGRTCVLSNLRGRTITTAIVRARMAEPSPFGFWSAMSE 205
Db 121 REYVNISAENAAAGSAQVREIILDGRTCVLSNLRGRTYFMVRRARMAEPSPFGFWSAMSE 180
QY 206 PVSLT 211
Db 181 PASLT 186

RESULT 4
ID 028206 PRELIMINARY; PRT; 229 AA.
AC 028206;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RX [1]
RP SEQUENCE FROM N.A.
RA TISSUE=BONE MARROW;
RA Suliman H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61399; AAB03871.1; -.
DR HSSP: P19235; IEBA.

```



```

Db      18  SDVFLALATGEPLNCSQFFEDLTFCWDEEAA--PSGYQLLYAVRGEKPRACPLYSQ 75
QY      64  PTARGAIRFWCSLPTAD-TSSFVPLELRITAA--GAPRFRVIRI-----NE 108
Db      76  SVPTFGRRYVCQPPADQEVLEFPFLHLMVKNVSLNQLIQLRVLEVDSEVCCPTLMNP 135
QY      109 VLLIDAVGLVARLADESGHVIRMLPPETPMTSHIRFELDISAGNAGSVQVRELLEG 168
Db      136  VPIVLDQF-PCVHPPTASQF-HGPVFTSPAGBAPF-----LTVKGS-----173
QY      169  RTEGVLSNLGRRTITIAVARARMAEPFGFMSMSEPVSL 209
Db      174  ---CLVSGLDAGKSYWLQLRSDQDGLKSGWSPVTV 211

RESULT 8
ID 075462 PRELIMINARY; PRT; 422 AA.
AC 075462;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.
GN CLF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Elson G.C.A., Grader P., Losberger P., Herren S., Gretener D.,
RA Menoud L.N., Wells T.N.C., Kosco-Villbois M.H., Gauchat J.F.;
RA "CLF-1, a Novel Soluble Protein Shares Homology With Members of the
RT Cytokine Type-1 Receptor Family.";
RL J. Immunol. 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Magrangeas F., Jacques Y., Minvielle S.;
RT "Cloning and expression of a novel soluble protein containing
RT hematopoietic cytokine receptor domains.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059293; AAC28335.1; -
DR EMBL; AF073515; AAD39681.1; -
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
KW Signal; Receptor.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 422 CYTOKINE-LIKE FACTOR-1.
SQ SEQUENCE 422 AA; 46301 MW; AD9DEFCB01B84228 CRC64;

Query Match 11.2%; Score 122.5; DB 4; Length 422;
Best Local Similarity 22.9%; Pred. No. 0.0011;
Matches 52; Conservative 36; Mismatches 84; Indels 55; Gaps 13;

QY 14 PEELCTEERLELDYCFEEEAASAGVPG-----NFSFQLEDEW---KICRL 60
Db 138 PVNISCWSKMKDLTCFMT-----PGAHGETFLHTNSLKKLR---WYGDNTEEE 186
QY 61 HOAPTARGAIRFWCSLPTADTSSFVPLELRITAA--GAPRFR-VRIHINEVLLDAPVG 117
Db 187 YHTVGPSS-----CHIP-KDLAFTPEYIWEATNRLGARSADVLTDIDVYTTDPDP 240
QY 118 L-VARLADESGHYVIRMLPPET-----PMTSHIRFELDISAGNAGSVQVRELLEG 171
Db 241 VHSVSVRGLELDQSLSVRWVSPALKDFLFOAKYQIRYREVDSSV-----DMRWVDVDSNQT 295
QY 172 CVLSNLGRRTITIAVARARMAEPFG-----GFSMSEPVSLT 211

```

```

Db      296  CRLAGLKEGTIVYQVRCN-----PFGIYGSKKAGINSEMSHPPTAAS 338
RESULT 9
ID 09JMS5 PRELIMINARY; PRT; 425 AA.
AC 09JMS5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE CLASS I CYTOKINE RECEPTOR.
GN ZCYTORS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Presnell S.R., Jellberg A.C., Gilbert T., Whitmore T.E.,
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178684; AAD54385.1; -
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
KW Receptor.
SQ SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

Query Match 11.1%; Score 121.5; DB 4; Length 422;
Best Local Similarity 22.9%; Pred. No. 0.0014;
Matches 52; Conservative 36; Mismatches 84; Indels 55; Gaps 13;

QY 14 PEELCTEERLELDYCFEEEAASAGVPG-----NFSFQLEDEW---KICRL 60
Db 138 PVNISCWSKMKDLTCFMT-----PGAHGETFLHTNSLKKLR---WYGDNTEEE 186
QY 61 HOAPTARGAIRFWCSLPTADTSSFVPLELRITAA--GAPRFR-VRIHINEVLLDAPVG 117
Db 187 YHTVGPSS-----CHIP-KDLAFTPEYIWEATNRLGARSADVLTDIDVYTTDPPE 240
QY 118 L-VARLADESGHYVIRMLPPET-----PMTSHIRFELDISAGNAGSVQVRELLEG 171
Db 241 VHSVSVRGLELDQSLSVRWVSPALKDFLFOAKYQIRYREVDSSV-----DMRWVDVDSNQT 295
QY 172 CVLSNLGRRTITIAVARARMAEPFG-----GFSMSEPVSLT 211
Db 296 CRLAGLKEGTIVYQVRCN-----PFGIYGSKKAGINSEMSHPPTAAS 338

RESULT 10
ID 09JMS5 PRELIMINARY; PRT; 425 AA.
AC 09JMS5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE CYTOKINE RECEPTOR LIKE MOLECULE 3 PRECURSOR.
GN CRLF1 OR CRLM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hiroshima T., Iwama A., Nakamura Y., Nakauchi H.;
RA "Cytokine receptor like molecule 3.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040038; BAA92777.1; -
DR HSSP; P16471; 1BP3.
DR MGD; MGI:1340030; Crlf1.

```

RP SEQUENC OF 61-395 FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=SCOTTISH BLACKFACE / ISOLATE M22/80; TISSUE=ANTERIOR PITUITARY
 RX MEDLINE=99049302; PubMed=9832462;
 RA Tortorese D.J., Brooks J., Ingleton P.M., McNeill A.S.;
 RT "Detection of prolactin receptor gene expression in the sheep
 RT pituitary gland and visualization of the specific translation of the
 RT signal in gonadotrophs.";
 RL Endocrinology 139:5215-5223(1998).
 RN [3]
 RP SEQUENCE OF 147-302 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=PERIAL LIVER, AND CORPUS LUTEUM.
 RA Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.;
 RT "Two forms of the prolactin receptor messenger ribonucleic acid are
 RT present in ovine fetal liver and adult ovary.";
 RL Endocrine 3:291-295(1995).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS, LONG ISOFORM (L-OPR) (SHOWN
 CC HERE), SHORT ISOFORM (S-OPR) AND SOLUBLE ISOFORM; ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED (LIVER,
 CC PITUITARY, ADRENAL GLAND, OVARY AND FETAL LIVER).
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 DR EMBL: AF041257; AAB96795.1; -
 DR EMBL: AF041977; AAB96820.1; -
 DR EMBL: AF041979; AAB97082.1; -
 DR EMBL: AF042358; AAB97744.1; -
 DR EMBL: AF042358; AAB97743.1; -
 DR EMBL: AF041978; AAB96965.1; -
 DR EMBL: Y10578; CAA71597.1; -
 DR EMBL: Y10808; CAA71766.1; -
 DR HSSP: P14787; IAN3.
 DR InterPro: IPR002996; CRJA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; FN3; 2.
 DR SMART: SM00060; FN3; 2.
 DR POSITIVE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN 1.
 DR

KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 Alternative splicing.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 581 PROLACTIN RECEPTOR.
 FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
 FT DOMAIN 123 227 FIBRONECTIN TYPE-III.
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 75 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 GOSPEKPLIKCRSPEKFTTCWMEFGADGGLPTNTLY
 FT VARSPLIC 24 66 RK -> ASLVPGKCSVCTYMAVPPVGLFLMYLCVDO
 FT VARSPLIC 67 581 YLLIVTYS (IN SOLUBLE ISOFORM).
 FT VARSPLIC 286 296 MISSING (IN SOLUBLE ISOFORM).
 FT VARSPLIC 297 581 KGSSELRRL -> ISQPSRLVSFV (IN SHORT
 FT CONFLICT 281 281 ISOFORM).
 FT CONFLICT 387 387 I -> V (IN AAB97743 AND AAB97744).
 FT CONFLICT 387 387 E -> K (IN REF. 2).
 SQ SEQUENCE 581 AA; 65235 MW; EC534FDE538837A0 CRC64;

Query Match 10.2%; Score 112.5; DB 6; Length 581;
 Best Local Similarity 22.2%; Pred. No. 0.015;
 Matches 49; Conservative 41; Mismatches 100; Indels 31; Gaps 11;

OY 6 ALLIANGPPE---LICTERLEDVCFEEAASAGV-GPGNFS-FSFOLEDEPKLCRLHQAPTARGAIR 61
 DB 19 ASLNGSPPEKPKRLICRSBGKFTFCWMEFGADGGL-PTNYLITRKEGE---TLIH 73
 OY 62 QAPTARGAIRFWSLPTADSSFVPLELRLTA-----ASGAPFRHVHINEVLLDAP 115
 DB 74 ECPDYKGTGPNCSYFSSKRYTSMKMYITVSAINOMGISSDPLY---VDVTVIVEDEPP 130
 OY 116 VGLVAVL---ADESGHVYINLPPETPMTS---HIRELIDISAGNGAGSVORELLEGR 169
 DB 131 VNLLELKHEDRKPYLIMKWSPTLTDVKSQWFSIQYEIRLKEKATD--WETHFAPKL 188
 OY 170 TECVLSNLRGRTRITTIIVARMAEPSPFGFMSAEPVSLL 210
 DB 189 TOLKIFNLPGQKLVQIRCK---PDH-GTWSEMS-PESEF 224

RESULT 13
 046600 PRELIMINARY; PRT; 634 AA.
 AC 046600;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE SOMATOTROPIN RECEPTOR 1B PRECURSOR.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HOLSTEIN;
 RA Lucy M.C., Boyd C.K.;
 RT "Bovine somatotropin receptor 1B mRNA."
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF044258; AAC02534.1; -.
 DR HSSP: P10912; 1A22.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN.1.

KW Signal; Receptor.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 634 SOMATOTROPIN RECEPTOR 1B.
 SQ SEQUENCE 634 AA; 70914 MW; 176936D32EA7C4C9 CRC64;

Query Match 10.2%; Score 112.5; DB 6; Length 634;
 Best Local Similarity 26.3%; Pred. No. 0.017;
 Matches 35; Conservative 25; Mismatches 60; Indels 13; Gaps 5;

OY 14 PEELICTERLEDVCFEEAASAGV-GPGNFS-FSFOLEDEPKLCRLHQAPTARGAIR 71
 DB 51 PKTKCSPELEFTSCWMTGAGNHSLOSQVGFYIRRIDQEKEC-----PDVVSAGE 105
 OY 72 FWSLPTADSSFVPLELRLTAASGAPFRHVHINEVLLDAPVGLVARLADES----- 126
 DB 106 NSCYFNSSVSWMPYCIRKILTSNGIYD-HKCFSEVDIVQDPDPVGLNWTLLNISTEIH 164
 OY 127 GHVYINLPPET 139
 DB 165 ADILVKNPEPPT 177

RESULT 14
 090MG7 PRELIMINARY; PRT; 626 AA.
 AC 090MG7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE PROLACTIN RECEPTOR PRECURSOR.
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Cynops.
 OX NCBI_Taxid=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Yamamoto T., Nakayama Y., Matsuda Y., Abe S.-I.;
 RT "Cloning and expression of a cDNA encoding a prolactin receptor of the
 RT Japanese red-bellied newt, Cynops pyrrhogaster."
 RL Zool. Sci. 15:741-747(1998).
 DR EMBL: AB005045; BAB61107.1; -.
 KW Signal; Receptor.
 FT SIGNAL 26
 SQ SEQUENCE 626 AA; 69944 MW; B6050DD9C9F58DE5 CRC64;

Query Match 10.2%; Score 111.5; DB 13; Length 626;
 Best Local Similarity 19.3%; Pred. No. 0.021;
 Matches 40; Conservative 42; Mismatches 88; Indels 37; Gaps 8;

OY 14 PEELICTERLEDVCFEEAASAGV-GPGNFS-FSFOLEDEPKLCRLHQAPTARGAIRFW 73
 DB 34 PVNIMCRSPEKFTSCWMPGSDGGL-PTNYSLLYKTEGK-----TSECPDYKTSFNS 88
 OY 74 CSLPTADSSFVPLEL-----RLTAASGAPFRHVHINEVLLDAPVGLVARLADES 127
 DB 89 CFEDKHTISWTWNINIVNATNELGSTDPKF---VDVAVIYQLRPLNWTLSIIEPP 145
 OY 128 HVTIRMLPPETPMTS---HIRELIDISAGN-----AGSVORVLLGGRRECVSNL 177
 DB 146 HLLVKNPSEADVKSGWVIEYVQFSKRAKEMETLTAGKOROLKVF-----SL 196
 OY 178 RGRTRITIVARMAEPSPFGFMSAMS 204
 DB 197 NPSENTIVQYRCK-----SDHGFSWMS 219

RESULT 15
 096TF0 PRELIMINARY; PRT; 521 AA.
 AC 096TF0;
 ID 096TF0;
 SQ SEQUENCE 521 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE INTERLEUKIN 9 RECEPTOR.
 GN IL9R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20122249; PubMed=10655549;
 RA Ciccodicola A., D'Esposito M., Esposito T., Gianfrancesco F.,
 RA Migliaccio C., Milano M.G., Matarazzo M.R., Vacca M., Franze A.,
 RA Cucurese M., Cocchia M., Curci A., Terracciano A., Torino A.,
 RA Cocchia S., Mercadante G., Pannone E., Archidiacono N., Rocchi M.,
 RA Schlessinger D., D'Urso M.;
 RT "Differentially regulated and evolved genes in the fully sequenced
 RT Xq/Yq pseudoautosomal region."
 RL Hum. Mol. Genet. 9:395-401(2000).
 DR EMBL: AJ271736; CAB96817.1; -.
 KW Receptor.
 SQ SEQUENCE 521 AA; 57146 MW; 07C40436466173F3 CRC64;

Query Match 10.1%; Score 111; DB 4; Length 521;
 Best Local Similarity 23.7%; Pred. No. 0.019; Indels 46; Gaps 11;
 Matches 53; Conservative 28; Mismatches 97;
 OY 12 RGPPEE-LLCFTEERLEDLVCFEEAASAGVGPNGFSFQLEDEPWKLCRLHQAPTARGA 69
 DB 47 QGPRSRRTFTCLNNILRIDCHW-SAPELGQG-----SSPWLLFTSNQAPGCTHK 94
 OY 70 IFNCSLPFADSSVPEPLERLTAASG-APRRHYIHINEV-----VLLDAP 115
 DB 95 ---CILRGSSECTVVLPEAVLVPDSNFTITFHCMGSGREOVSLVDPEYLPRRHVKLDPP 150
 OY 116 VGLVARLADSGHVYLRW-LPPPEPMTSHIRFELDLSAGNGA-GSVORVELLEGTECV 173
 DB 151 SDLOSNIS--SGHCILTNWISPALEPMITLLSYELAFKQEPNWEQAQHRDHIVGTWLI 208
 OY 174 LSNL-----RGRRTITIAVRAR-MAEPSGFGFWSAMSEPV 207
 DB 209 LEAFELDPGFIEARLRVQMATLEDVDVEEERYTGQWSEMSQPV 252

Search completed: August 28, 2002, 17:40:15
 Job time: 546 sec

THIS PAGE BLANK (USPTO)